

Resource Summary Report

Generated by [NIF](#) on Sep 2, 2026

GARM

RRID:SCR_006731

Type: Tool

Proper Citation

GARM (RRID:SCR_006731)

Resource Information

URL: <http://garm-meta-assem.sourceforge.net/>

Proper Citation: GARM (RRID:SCR_006731)

Description: A new software pipeline to merge and reconcile assemblies from different algorithms or sequencing technologies.

Abbreviations: GARM

Synonyms: Genome Assembler Reconciliation and Merging

Resource Type: software resource

Resource Name: GARM

Resource ID: SCR_006731

Alternate IDs: OMICS_01420

Record Creation Time: 20220129T080237+0000

Record Last Update: 20260829T182243+0000

Ratings and Alerts

No rating or validation information has been found for GARM.

No alerts have been found for GARM.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 12 mentions in open access literature.

Listed below are recent publications. The full list is available at [NIF](#) .

Zhu D, et al. (2025) Gradient-aware modeling advances AI-driven prediction of genetic perturbation effects. *bioRxiv : the preprint server for biology*.

Hayden NK, et al. (2023) Reducing the risk of criminal exploitation using multi-systemic therapy (the RESET Study): study protocol for a feasibility study and process evaluation. *Pilot and feasibility studies*, 9(1), 193.

Vong K, et al. (2021) Disrupting tumor onset and growth via selective cell tagging (SeCT) therapy. *Science advances*, 7(17).

Gupta A, et al. (2021) Evaluation of immediate and short-term efficacy of DualStim therapy with and without intracavernosal umbilical cord-derived Wharton's jelly in patients with erectile dysfunction: Study protocol for a randomized controlled trial. *Contemporary clinical trials communications*, 23, 100790.

Kim J, et al. (2020) Whole-genome, transcriptome, and methylome analyses provide insights into the evolution of platycoside biosynthesis in *Platycodon grandiflorus*, a medicinal plant. *Horticulture research*, 7, 112.

Nicholson TL, et al. (2020) Comparative Virulence and Genomic Analysis of *Streptococcus suis* Isolates. *Frontiers in microbiology*, 11, 620843.

Nielsen ES, et al. (2020) Multi-model seascape genomics identifies distinct environmental drivers of selection among sympatric marine species. *BMC evolutionary biology*, 20(1), 121.

de Souza WM, et al. (2019) Pingu virus: A new picornavirus in penguins from Antarctica. *Virus evolution*, 5(2), vez047.

Modha S, et al. (2019) Metaviromics Reveals Unknown Viral Diversity in the Biting Midge *Culicoides impunctatus*. *Viruses*, 11(9).

Solrzano S, et al. (2019) De Novo Assembly Discovered Novel Structures in Genome of Plastids and Revealed Divergent Inverted Repeats in *Mammillaria* (Cactaceae, Caryophyllales). *Plants (Basel, Switzerland)*, 8(10).

Gokul EA, et al. (2019) Remotely sensing harmful algal blooms in the Red Sea. *PloS one*, 14(4), e0215463.

Leijs R, et al. (2015) The Evolution of Epigeal and Stygobitic Species of *Koonunga* Sayce, 1907 (Syncarida: Anaspidacea) in Southern Australia, with the Description of Three New Species. *PloS one*, 10(8), e0134673.